

logo

NTDB id 358864 E8M06 RS09175 WP 136581540.1
NTDB id 463 GPW51 RS08685 WP 012775331.1
consensus

80
80

logo

NTDB id 358864 E8M06 RS09175 WP 136581540.1
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consensus

FGGMVDIS^MFGYD^DERKLDDSGLAKAEFDV^KGKKITVSLTGKDYK^SWSDG^QESFTINDYIFTIKSMASKDYTG^RVRFD^KDFLN
 FGGMVDIS^MFGYD^DERKLDDSGLAKAEFDV^KGKKITVSLTGKDYK^SWSDG^QESFTINDYIFTIKSMASKDYTG^RVRFD^KDFLN
 FGGMVDIS^MFGYD^DERKLDDSGLAKAEFDV^KGKKITVSLTGKDYK^SWSDG^QESFTINDYIFTIKSMASKDYTG^RVRFD^KDFLN

160
160

logo

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240
240

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I K E I V N G E S I T Y V P N E Y F F K G T _k P K T S S L K I D I V S P D T I V S E M K A G N Y D I A E M P V D Q L D S Y K D A S N L N I V G S L E S S Y E Y I
 I K E I V N G E S I T Y V P N E Y F F K G T P K T S S L K I D I V S P D T I V S E M K A G N Y D I A E M P V D Q L D S Y K D A S N L N I V G S L D S A Y E Y I
 I K E I V N G E S I T Y V P N E Y F F K G T K P K T S S L K I D I V S P D T I V S E M K A G N Y D I A E M P V D Q L D S Y K D A S N L N I V G Q L E S S Y E Y I

320
320

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Sequence alignment:

SFNV	E	GKYDE	A	A	GKNVMDENAKMNDVKLRQAIAYAIDTKTAG	K	E	SLYNGLYHPA	N	SLIISFFGDIHDSELEGYSYNPEKAKK
SFNL	L	GKYDES	A	A	GKNVMDENAKMNDVKLRQAIAYAIDTKTAG	E		SLYNGLYHPAN		SLIISFFGDIHDSELEGYSYDPEKAKK
SFN	F	GKYDEA	A	A	GKNVMDENAKMNDVKLRQAIAYAIDTKTAG	K		SLYNGLYHPAK	K	SLIISFFGDIHDSELEGYSYNPEKAKK

400
400

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LL^EEAGYKDV^DDGD^GGIREGKD^GGK^EE^FKTFAARKRTEANEALVQ^YYIAW^KKEVGLNVELYTGRTVE^INT^FYEA^VQAND^PPAID
 LL^EEAGYKDV^DDGD^GGIREGKD^GGK^EE^FKTFAARKRTEANEALVQ^YYIAW^KKEVGLNVELYTGRTVE^INT^FYEA^VQAND^PPAID
 LL^EEAGYKDV^DDGD^GGIREGKD^GGK^EE^FKTFAARKRTEANEALVQ^YYIAW^KKEVGLNVELYTGRTVE^INT^FYEA^VQAND^PPAID
 * * * * *

480
480

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560
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consensus

YVNRVKSYDINYSASGKGLAYENIELTADKGWAE

LNKRVKNYDSNYGSASGKGLAYENIELTADKGVVAE

VNKRVKSYDTKYGSASGTGLAYEGIELTADKGVVAE

!!!!!! !! !!!!!!! !*! ! !!!!!!!

596

596

- X

 non conserved
- X

 similar
- X

 ≥ 50% conserved